

# **SARS-CoV-2 Sequencing and Variants in Washington State**

**Washington State Department of Health**

**March 30, 2022**

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# **SARS-CoV-2 Sequencing and Variants in Washington State**

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Next generation sequencing is a set of laboratory methods that scientists use to scan a viral genome to determine the genome sequence of a virus. A genome sequence of a virus is referred to as its “genomic fingerprint,” and can reveal mutations in a virus that make it unique. Mutations are changes in a genome sequence and occur naturally over time.

Scientists compare viral genomes to better understand how viruses can spread from person to person. Sequencing allows public health officials to detect clusters of cases, and monitor new lineages. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage. Some lineages may have characteristics such as the ability to spread more quickly, or cause more severe disease. These lineages are classified as variants of interest, variants being monitored, or variants of high concern.

Throughout this report, we refer to the scientific name of the virus SARS-CoV-2 that causes COVID-19. Sequencing can only be performed on samples that are processed in laboratories and where swabs are stored in liquid that is compatible with sequencing, which means only samples used for molecular tests (such as PCR) can be included. For this reason, this report is limited to confirmed cases only. The genomes that are sequenced and compared are those of the virus, not humans.

### **At a glance (data through March 29, 2022)**

- During the month of February 2022, **8.9%** of all confirmed molecular COVID-19 cases were sequenced. This number is preliminary and will change over time as additional specimens are received from the previous month.
- **81,375 (8.3%)** COVID-19 cases in Washington state have sequencing information available since January 2021.

CDC currently categorizes variants as Variants of High Consequence (VOHC), Variants of Concern (VOC), Variants of Interest (VOI) and Variants Being Monitored (VBM). There are currently no VOHC and VOI so only VOC and VBM are detailed in this report.

## Variants of Concern

Variant	Area first detected	Background	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Delta (B.1.617.2 and AY lineages)	India	Delta has been found to be more transmissible than other variants such as Alpha, and some research indicates greater risk of hospitalization. Approved vaccines are effective at preventing severe disease and death, including against the Delta variant.	38,057	Apr 03, 21	Feb 21, 22
Omicron (B.1.1.529 and BA lineages)	South Africa	Early research indicates evidence for increased transmissibility, immune evasion, and lower risk of hospitalization and death, relative to Delta. Approved vaccines are effective at preventing severe disease and death, including against the Omicron variant.	20,127	Nov 29, 21	Mar 19, 22

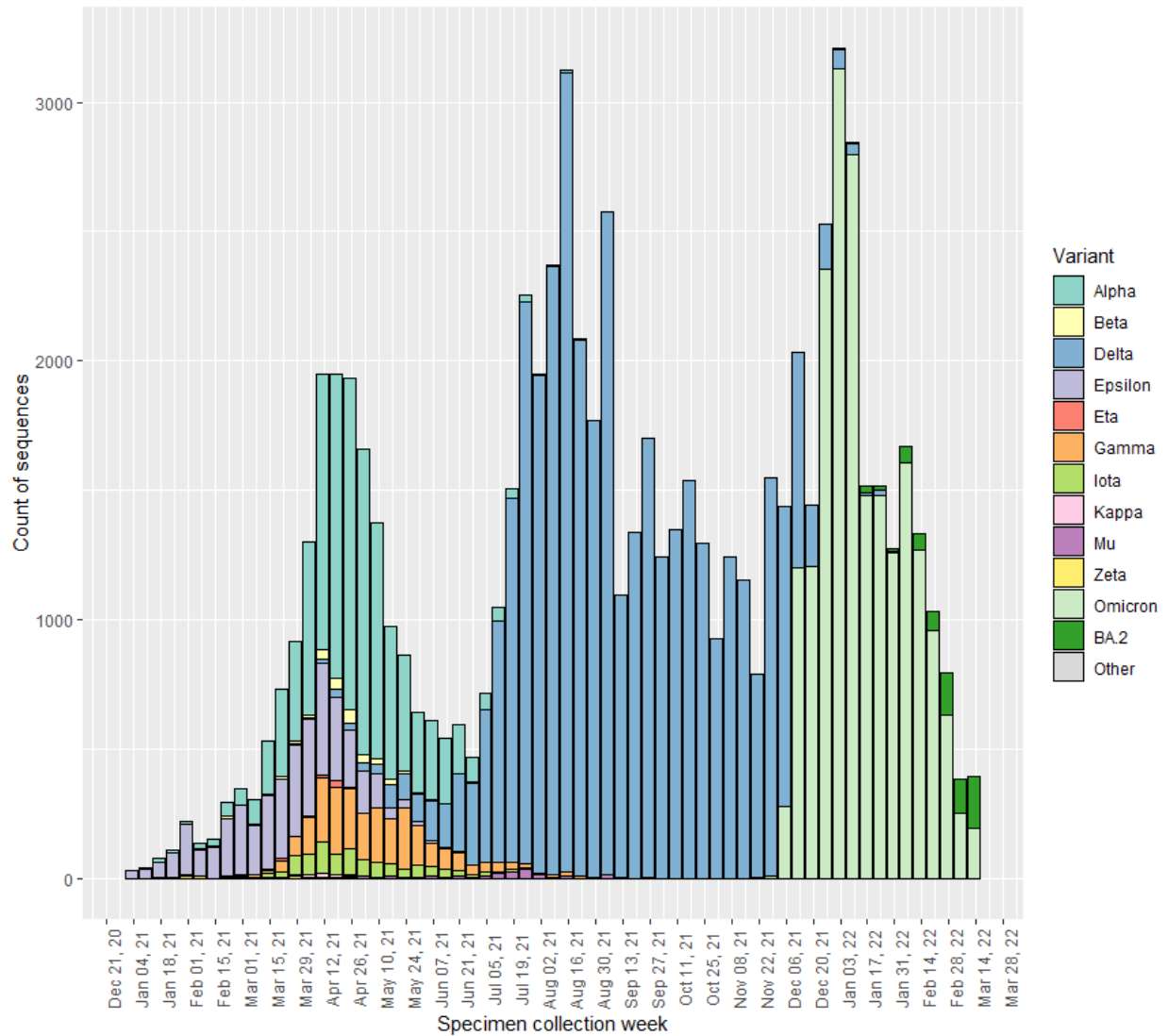
\*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

## Variants being monitored

Variant	Area first detected	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Alpha (B.1.1.7)	United Kingdom	9,931	Jan 07, 21	Sep 08, 21
Beta (B.1.351)	South Africa	272	Jan 29, 21	Jun 29, 21
Epsilon (B.1.427 / B.1.429)	California	4,042	Dec 11, 20	Jun 24, 21
Eta (B.1.525)	New York	83	Feb 02, 21	Jun 08, 21
Gamma (P.1)	Brazil	2,399	Feb 06, 21	Dec 02, 21
Iota (B.1.526)	New York	894	Jan 21, 21	Aug 20, 21
Kappa (B.1.617.1)	India	46	Mar 22, 21	Jun 14, 21
Mu (B.1.621)	Colombia	183	Apr 09, 21	Dec 20, 21
Zeta (P.2)	Brazil	44	Jan 18, 21	Apr 20, 21

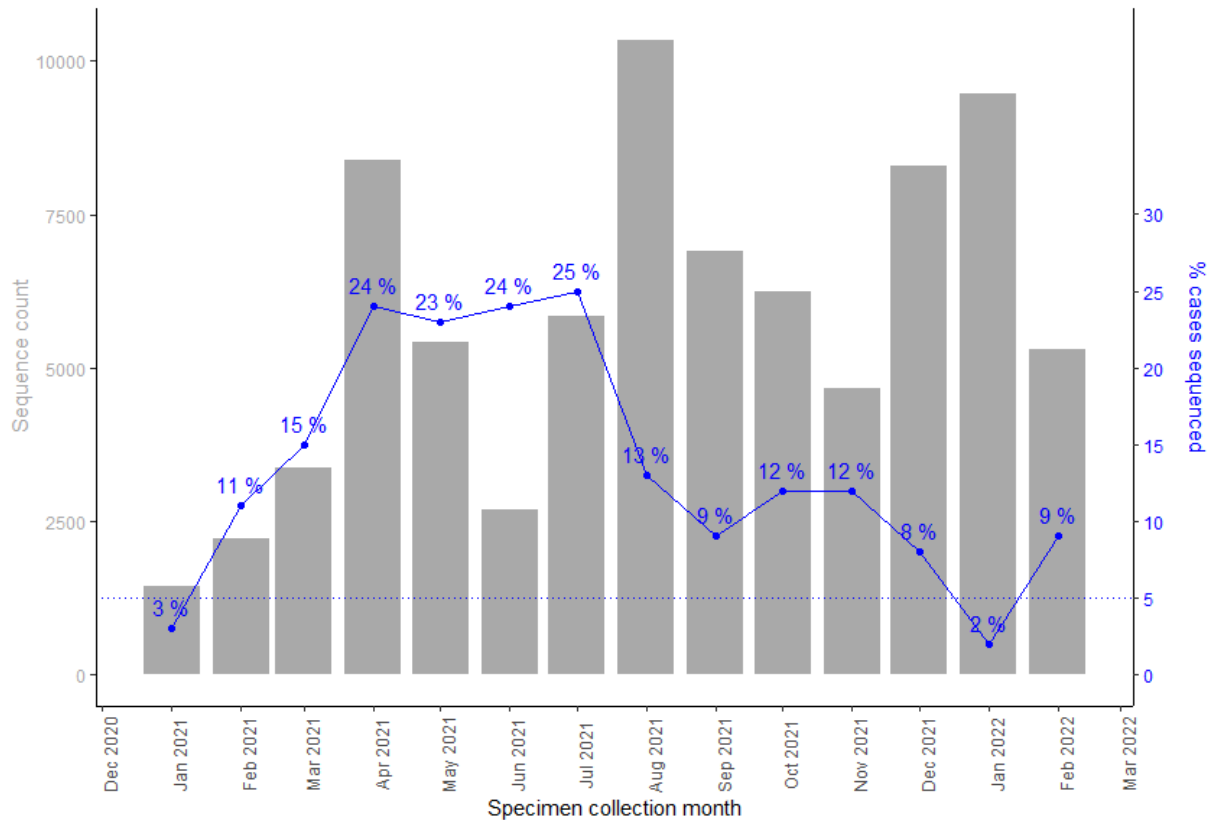
\*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

## Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to March 19, 2022



- The above graph shows the total number of variants detected by the week the specimen was collected from a patient.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.
- This graph shows all specimens sequenced, including specimens sequenced during outbreaks and other targeted sequencing efforts.

**Number of specimens sequenced, and percent of Washington State confirmed COVID-19 cases that have been sequenced by specimen collection date from January 2021 through February 2022.**

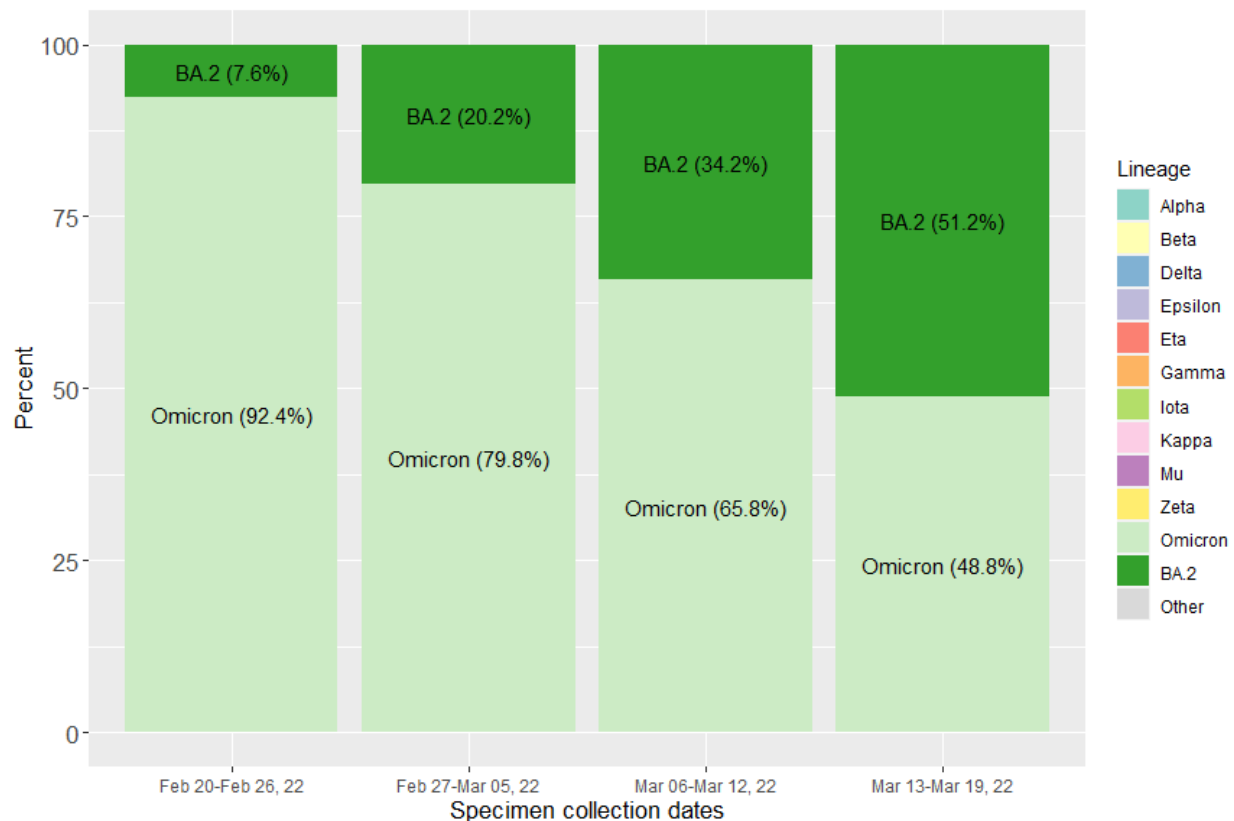


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing can be performed on stored specimens at any time, so numbers from past months may change if stored specimens are sequenced.

## SARS-CoV-2 Lineages Circulating in Washington State

The graph below shows the change in proportion of select SARS-CoV-2 lineages by time period. A viral lineage is a group of viruses that descend from a common ancestor with shared genetic characteristics, allowing them to be grouped together. There are many different virus lineages that are not variants of concern or variants being monitored. These are grouped together as 'Other' on this chart. As the proportions of variants increase, the proportion of other lineages will decrease.

NOTE: The data on this graph come from cases that are randomly selected for sequencing statewide; cases sequenced because they were part of an outbreak or were otherwise manually selected for sequencing are excluded.



- The chart above shows the proportions of the most common SARS-CoV-2 lineages circulating in Washington grouped in one-week intervals. Proportions are calculated using data which are subject to change over time and will be updated as more data becomes available, including data from prior time periods. **Due to the time it takes to complete sequencing, the most recent time period is based on a very small number of sequences and likely to be adjusted over time.**

To see the national trends, visit the CDC's [variant proportions page](#).

**The table below shows the number of variants of concern (VOC) and variants being monitored (VBM) detected by county of home address since January 2021.**

	VOC		VBM									
County	Delta	Omicron	Alpha	Beta	Gamma	Epsilon	Eta	Iota	Kappa	Mu	Zeta	Total specimens sequenced
Adams	280	60	34	0	3	18	0	2	0	0	0	397
Asotin	89	13	8	0	0	0	0	1	0	0	0	111
Benton	2,115	589	414	1	85	230	22	71	0	17	0	3,544
Chelan	427	191	30	0	2	8	0	0	0	0	0	658
Clallam	649	259	75	0	20	5	0	1	0	22	0	1,031
Clark	731	376	99	1	40	31	0	3	0	0	0	1,281
Columbia	2	6	0	0	0	0	0	0	0	0	0	8
Cowlitz	716	291	47	0	42	27	0	1	0	0	0	1,124
Douglas	260	119	23	0	0	6	0	4	0	1	0	413
Ferry	27	8	3	0	0	1	0	0	0	0	0	39
Franklin	1,547	372	316	4	107	168	12	35	0	11	1	2,573
Garfield	15	0	0	0	0	0	0	0	0	0	0	15
Grant	777	232	67	0	15	26	1	6	0	0	0	1,124
Grays Harbor	348	425	46	2	15	21	0	0	0	0	0	857
Island	251	83	34	0	7	2	0	0	0	0	0	377
Jefferson	127	76	28	0	0	6	0	3	0	0	0	240
King	11,647	8,475	5,044	192	1,062	1,847	32	440	37	71	30	28,877
Kitsap	392	305	60	2	6	33	0	6	0	2	0	806
Kittitas	375	71	29	1	16	7	0	1	0	6	0	506
Klickitat	112	21	7	0	3	1	0	5	0	0	0	149
Lewis	759	174	74	0	8	22	0	0	0	0	1	1,038
Lincoln	71	6	5	0	2	1	0	1	0	0	0	86
Mason	138	69	23	1	3	3	0	3	0	0	0	240
Okanogan	213	80	15	0	0	2	0	0	0	1	0	311

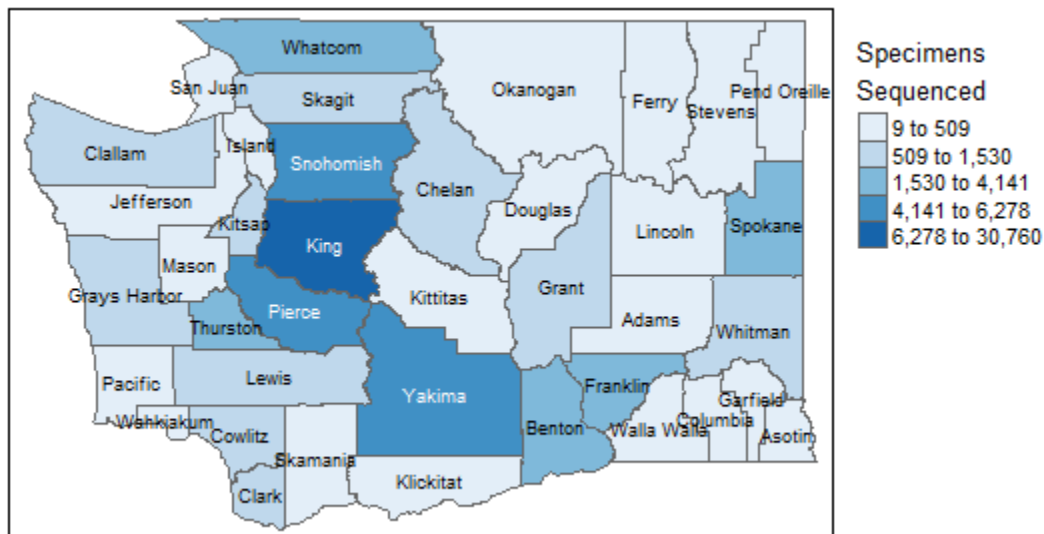


	VOC		VBM									
County	Delta	Omicron	Alpha	Beta	Gamma	Epsilon	Eta	Iota	Kappa	Mu	Zeta	Total specimens sequenced
Pacific	187	126	20	0	7	29	0	0	0	0	0	369
Pend Oreille	86	12	2	0	2	0	0	3	0	0	0	105
Pierce	2,232	1,506	871	24	148	463	2	78	0	19	3	5,346
San Juan	29	10	6	0	0	0	0	0	0	0	0	45
Skagit	1,018	265	179	1	35	20	0	1	0	0	0	1,519
Skamania	15	7	3	0	0	0	0	2	0	0	0	27
Snohomish	2,760	1,291	1,180	21	226	354	6	42	6	8	1	5,895
Spokane	2,741	671	192	1	129	56	4	52	1	0	0	3,847
Stevens	153	26	15	0	4	1	0	2	1	0	0	202
Thurston	1,188	1,300	143	4	13	49	0	6	0	1	0	2,704
Wahkiakum	22	6	7	0	2	0	0	0	0	0	0	37
Walla Walla	275	157	9	0	5	13	1	3	0	10	0	473
Whatcom	2,095	844	476	6	256	37	2	21	1	5	0	3,743
Whitman	539	210	71	0	13	13	0	6	0	0	0	852
Yakima	2,553	1,349	249	10	108	493	1	92	0	8	8	4,871

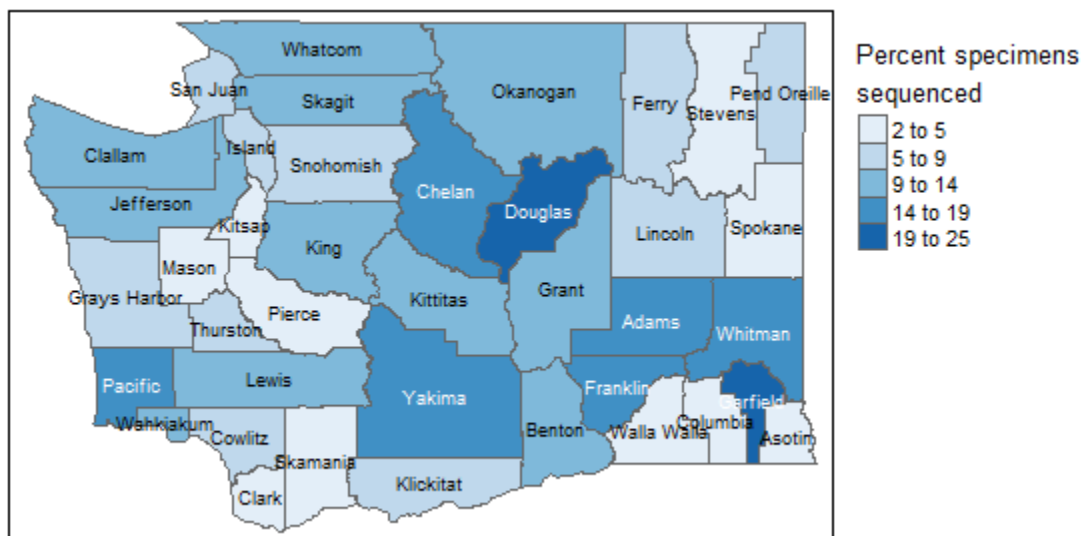
## Geographic Coverage of Sequencing

Efforts are made to sequence specimens from all geographic areas of Washington State. The number of sequences and the percent of cases sequenced vary based on several factors including which laboratories conduct the majority of testing in each locality.

**The map below shows the number of specimens sequenced by county of home address since January 1, 2021.**



**The map below shows the percent of COVID-19 cases with at least one specimen sequenced by county of home address since January 1, 2021.**



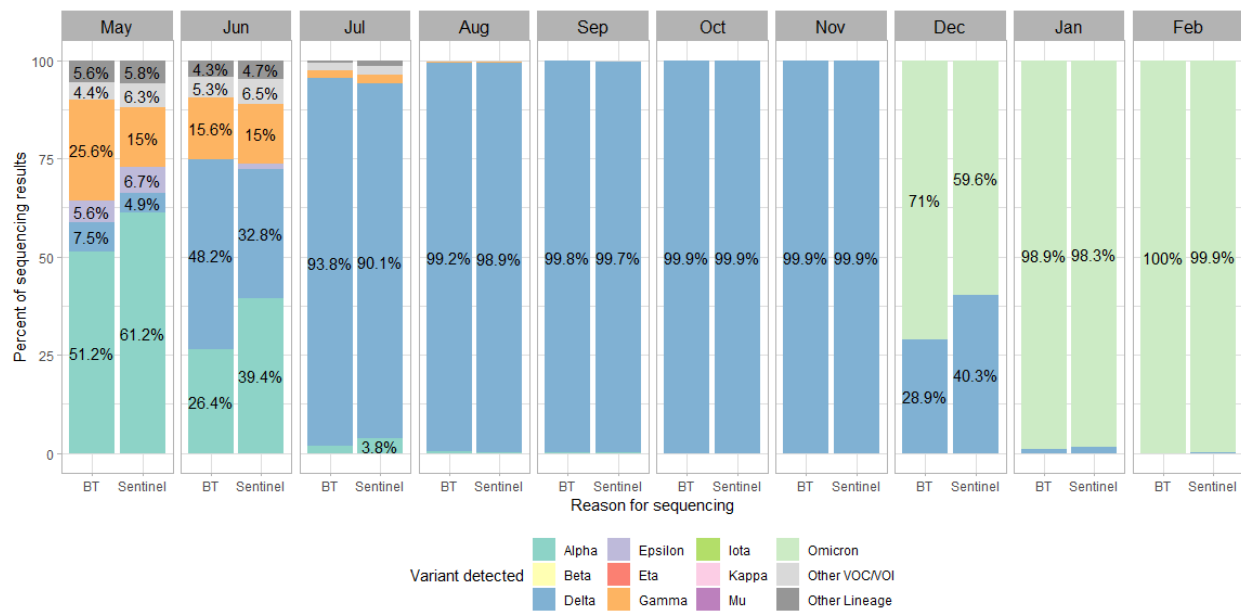
## Vaccine Breakthrough Cases

A complete report on vaccine breakthrough cases can be found in the reports section of the [DOH data dashboard](#).

A vaccine breakthrough case is defined as someone who tests positive for SARS-CoV-2 at least 14 days after their final dose of SARS-CoV-2 vaccine. DOH is monitoring sequencing results for vaccine breakthrough cases. This can help scientists determine whether any specific variants of the virus are causing more breakthrough cases than expected.

The table and chart below show vaccine breakthrough cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'other'.

**Proportion of variants identified among vaccine breakthrough cases (Breakthrough) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame**



## Breakthrough cases by variant table

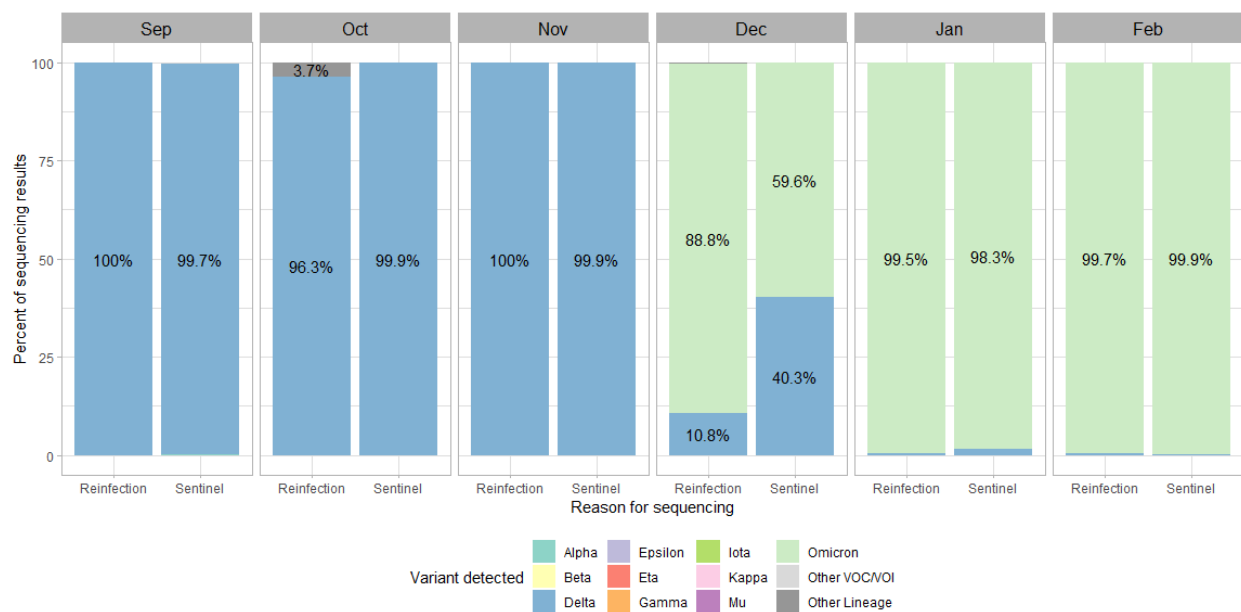
Variant	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar
Alpha	138	164	105	30	9	1	0	0	0	0	0	0
Delta	3	24	192	1,651	2,931	2,013	2,170	1,643	1,281	56	0	0
Epsilon	81	18	1	0	0	0	0	0	0	0	0	0
Gamma	53	82	62	33	6	0	0	0	1	0	0	0
Omicron	0	0	0	0	0	0	0	1	3,151	5,104	2,992	905
Other VOC/VOI	21	14	21	34	6	3	0	0	0	0	0	0
Other Lineage	27	18	17	13	4	0	2	1	3	2	0	0

## Reinfection

A complete report on reinfection cases can be found in the reports section of the DOH data dashboard.

In general, reinfection means a person was infected once with the virus that causes COVID-19, recovered, and then later became infected again. We are still learning about COVID-19 and the duration and strength of immunity following infection with this virus. Based on what we know from similar respiratory viruses, we expect some COVID-19 reinfections to occur. For disease surveillance purposes, a person with a reported reinfection is an individual with two positive COVID-19 test results (molecular or antigen) reported to DOH where the tests were performed at least 90 days apart. In addition, if genetic sequencing of respiratory samples from a patient's first (or primary) infection and most recent infection identifies different variants, they are considered a confirmed reinfection regardless of the amount of time between positive tests. Washington State Department of Health adopted this definition on September 1, 2021.

DOH is monitoring sequencing results for reinfection cases. This can help scientists determine whether any specific variants of the virus are causing more reinfection cases than expected. The table and chart below show reinfection cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'other'. Proportion of variants identified among reinfection cases (Reinfection) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame.



## Reinfection cases by variant table

Please note - data for the most recent month are incomplete

Variant	Sep	Oct	Nov	Dec	Jan	Feb	Mar
Delta	32	52	46	28	2	1	0
Omicron	0	0	0	231	587	288	18
Other Lineage	0	2	0	1	1	0	0

## Symptom information

Public Health gathers information from patients during interviews and records information about what symptoms people experience during their illness. Not all patients are able to be interviewed, so the symptom status is 'unknown' for many cases of illness. When there are a lot of infections, it is more challenging to contact each person, which is why some variants such as Delta have information available for a smaller percentage of cases. Information in the tables below is only presented for variants with at least 100 cases identified.

### Symptom status by variant

	VOC		VBM						
Symptoms	Delta	Omicron	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Yes	89%	69%	91%	86%	91%	92%	92%	85%	91%
No	11%	31%	9%	14%	9%	8%	8%	15%	9%
Unknown	48%	81%	34%	31%	35%	31%	36%	37%	41%
Total cases	37,961	19,652	9,904	271	3,993	2,384	891	182	5,749

### Symptoms by variant among cases reporting symptoms

	VOC		VBM						
Symptom	Delta	Omicron	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Total symptomatic	17,564	2,636	5,941	161	2,359	1,514	527	98	3,117
Fever	49%	51%	33%	20%	26%	38%	31%	30%	31%
Muscle aches	45%	49%	32%	20%	27%	34%	29%	29%	33%
Sore throat	38%	59%	27%	20%	21%	26%	29%	29%	25%
Cough	62%	70%	40%	26%	31%	42%	41%	41%	37%
Shortness of breath	17%	16%	12%	10%	11%	14%	9%	13%	12%
Nausea or vomiting	18%	18%	12%	10%	10%	14%	13%	10%	11%
Headache	55%	57%	38%	24%	33%	38%	34%	44%	39%
Abdominal pain	11%	10%	8%	7%	7%	8%	5%	9%	9%
Diarrhea	18%	14%	12%	6%	10%	13%	10%	10%	12%
Loss of taste or smell	43%	16%	21%	16%	24%	24%	24%	31%	29%

\*Other includes all viruses that are not categorized as VOC or VBM

The hospitalization table below does not account for factors that can influence hospitalization rates such as age and vaccination status, which may be different across variants. This means that hospitalization rates are not necessarily comparable between variants.

### Hospitalizations and deaths by variant

	VOC		VBM						
Outcome	Delta	Omicron	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Cases who were hospitalized	4.2%	1.2%	3.3%	6.3%	2.5%	6.7%	3.1%	3.3%	2.4%
Cases who died from COVID-19	1.2%	0.3%	0.5%	0.4%	0.7%	1.6%	1.1%	2.2%	0.7%
Total cases	37,961	19,652	9,904	271	3,993	2,384	891	182	5,749

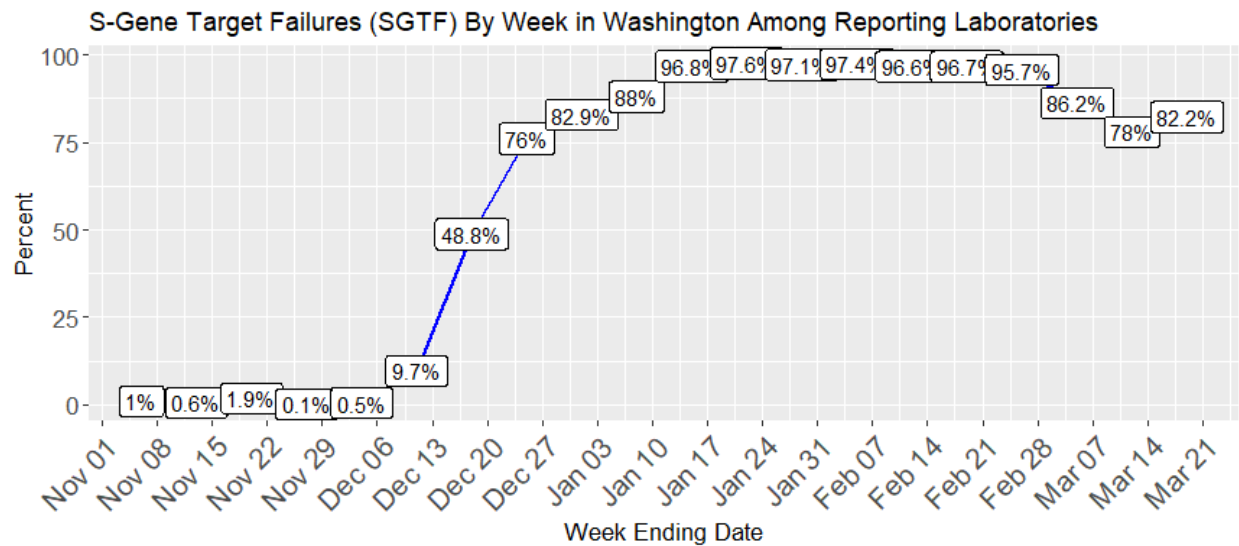
### Age distribution by variant

	VOC		VBM						
Age group	Delta	Omicron	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Age 0-19	23%	24%	27%	30%	25%	22%	25%	23%	24%
Age 20-34	29%	32%	32%	35%	31%	35%	32%	37%	30%
Age 35-49	22%	22%	22%	21%	22%	23%	24%	19%	23%
Age 50-64	14%	13%	12%	11%	14%	11%	12%	12%	15%
Age 65-79	7%	5%	3%	3%	4%	4%	4%	6%	5%
Age 80+	2%	2%	1%	0%	1%	3%	1%	1%	1%
Unknown	2%	2%	2%	1%	2%	2%	1%	2%	2%
Total cases	37,961	19,652	9,904	271	3,993	2,384	891	182	5,749

\*Other includes all viruses that are not categorized as VOC or VBM

## Tracking Omicron Using Clinical Tests

WA DOH is tracking the Omicron variant using sequencing. One challenge is that the sequencing process can take up to a few weeks, so we use another testing marker known as 'S gene target failure (SGTF)' to identify possible Omicron cases carrying this mutation rapidly and inform public health action. While SGTF does not always mean that a case will be finalized as omicron, greater than 95% of these results are predicted to finalize as omicron. Many laboratories are sharing this data with WA DOH to help track the spread of Omicron.



A small number of other SARS-CoV-2 viruses other than Omicron can cause SGTF, these can be seen in the small numbers (0-3) seen weekly prior to the week of November 28th. Additionally, the Omicron sub-lineage BA.2 does not carry this mutation.

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2021-10-31	2021-11-06	1,282	13	1%
2021-11-07	2021-11-13	1,278	8	0.6%
2021-11-14	2021-11-20	1,286	24	1.9%
2021-11-21	2021-11-27	1,389	2	0.1%
2021-11-28	2021-12-04	2,619	13	0.5%
2021-12-05	2021-12-11	2,514	243	9.7%
2021-12-12	2021-12-18	3,356	1,637	48.8%
2021-12-19	2021-12-25	5,309	4,034	76%
2021-12-26	2022-01-01	6,786	5,625	82.9%
2022-01-02	2022-01-08	16,159	14,218	88%
2022-01-09	2022-01-15	17,156	16,599	96.8%
2022-01-16	2022-01-22	13,822	13,494	97.6%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2022-01-23	2022-01-29	9,108	8,848	97.1%
2022-01-30	2022-02-05	4,968	4,840	97.4%
2022-02-06	2022-02-12	2,794	2,700	96.6%
2022-02-13	2022-02-19	1,433	1,385	96.7%
2022-02-20	2022-02-26	674	645	95.7%
2022-02-27	2022-03-05	508	438	86.2%
2022-03-06	2022-03-12	236	184	78%
2022-03-13	2022-03-19	253	208	82.2%

We thank the reporting laboratories: University of Washington Virology, Northwest Laboratories, The Vancouver Clinic, Atlas Laboratories, Evergreen Health, FidaLab



We gratefully acknowledge the GISAID initiative, original laboratories responsible for obtaining the specimens, as well as the submitting laboratories where the genome data were generated and shared via GISAID.

**The following clinical laboratories have contributed specimens for sequencing:**

Aegis Sciences Corporation  
Allenmore Hospital Laboratory  
Altius Institute for Biomedical Sciences  
Atlas Genomics  
BioReference Laboratories Inc.  
Cascade Valley Hospital  
Central Washington Hospital  
Columbia Basin Hospital  
Curative Labs Inc.  
Dayton General Hospital  
Deaconess Hospital  
Diatherix Laboratories  
Dynacare Northwest Inc.  
East Adams Rural Hospital  
Everett Clinic Microbiology  
Evergreen Healthcare  
Ferry County Hospital  
FidaLab  
Forks Community Hospital  
Fulgent Genetics  
Gravity Diagnostics, LLC  
Harborview Medical Center  
Healthquest Esoterics  
Helix/Illumina  
Incyte Diagnostics Spokane

Infinity Biologix  
Interpath Laboratory  
Jefferson Healthcare  
Kaiser Permanente Washington Health Research Institute  
Laboratories Northwest  
Laboratory Corporation of America  
Legacy Laboratory  
Magnolia Diagnostics, LLC  
Mann-Grandstaff VA Medical Center  
Mason General Hospital Laboratory  
Mid Valley Hospital  
Molecular Testing Labs  
MultiCare  
Northwest Laboratories  
Northwest Laboratories  
OHSU Lab Services Molecular Microbiology Lab  
Olympic Medical Center  
Overlake Hospital  
PeaceHealth  
Polyclinic  
Providence Regional Medical Center Everett  
Providence Sacred Heart Medical Center  
Public Health Seattle-King County Laboratory  
Quest Diagnostics Incorporated  
Samaritan Hospital Lab  
Seattle Children's Hospital  
Seattle Flu Study  
Skagit Valley Hospital Laboratory

St. Joseph Medical Center Microbiology  
St. Michael Medical Center Laboratory  
Swedish Medical Center  
The Vancouver Clinic  
Tomorrow's Health, LLC  
TridentCare Laboratory  
University of Washington Virology Lab  
Virginia Mason Franciscan Health Microbiology  
Washington State Department of Health Public Health Laboratories

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**The following labs have reported sequencing data that is included in this report:**

Aegis Laboratory  
Altius Institute for Biomedical Research  
Atlas Genomics  
Boise VA Medical Center  
Centers for Disease Control and Prevention  
Curative  
Flow Diagnostics  
Fulgent Genetics  
Ginkgo Bioworks Clinical Laboratory  
Gravity Diagnostics, LLC  
Gritman Medical Center  
Grubaugh Lab  
Helix Laboratories  
Idaho Bureau of Laboratories  
Infinity Biologix  
Institute for Systems Biology  
Kaiser Permanente  
Laboratory Corporation of America

Montana Public Health Laboratory  
Naval Health Research Center  
Oregon SARS-CoV-2 Genome Sequencing Center  
Oregon State Public Health Laboratory  
Providence St. Joseph Health Molecular Genomics Laboratory  
Quest Diagnostics  
Seattle Flu Study  
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